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RAW SEQUENCE LISTING PATENT APPLICATION US/08/882,435

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This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING 1 ENTERED 2 (1) General Information: 3 (i) APPLICANT: Hoxie, James A. 5 (ii) TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST CELLULAR 8 CORECEPTORS FOR HUMAN IMMUNODEFICIENCY VIRUS AND METHODS 9 OF USING THE SAME 10 11 (iii) NUMBER OF SEQUENCES: 6 12 13 (iv) CORRESPONDENCE ADDRESS: 14 (A) ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C. 15 (B) STREET: One Commerce Square, 2005 Market Street, 22nd Floor 16 (C) CITY: Philadelphia 17 (D) STATE: Pennsylvania 18 (E) COUNTRY: U.S. (F) ZIP: 19103-7086 19 20 (v) COMPUTER READABLE FORM: 21 (A) MEDIUM TYPE: Floppy disk 22 (B) COMPUTER: IBM PC compatible 23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS 24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 25 26 (vi) CURRENT APPLICATION DATA: 27 (A) APPLICATION NUMBER: US 08/882,435 28 29 (B) FILING DATE: 25-JUN-1997 30 (C) CLASSIFICATION: 31 32 (viii) ATTORNEY/AGENT INFORMATION: 33 (A) NAME: Doyle Leary, Ph.D., Kathryn (B) REGISTRATION NUMBER: 36,317 34 (C) REFERENCE/DOCKET NUMBER: 9596-11U1 35 36 (ix) TELECOMMUNICATION INFORMATION: 37 (A) TELEPHONE: 215-965-1284 38 (B) TELEFAX: 215-567-2991 39 40 (C) TELEX: 831-494 41 42 (2) INFORMATION FOR SEQ ID NO:1: 43 44 45 (i) SEOUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

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			INFUI SEI: 32930.74W
47 48 49 50		(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
51 52	(ii)	MOLECULE TYPE: DNA (genomic)	
53	(iii)	HYPOTHETICAL: NO	
54 55 56 57 58	(iv)	ANTI-SENSE: NO	
59 60 61	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:1:	
62 63	TAGATATC	TT ACCATGGAGG GGATCAG	27
64	(2) INFO	RMATION FOR SEQ ID NO:2:	
65 66 67 68 69 70	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 28 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
71 72 73	(ii)	MOLECULE TYPE: DNA (genomic)	
74 75	(iii)	HYPOTHETICAL: NO	
76 77 78 79	(iv)	ANTI-SENSE: NO	
80 81 82	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:2:	
83 84	TAGCGGCG	CT TAGTGGAGTG AAAACTTG	28
85 86	(2) INFO	RMATION FOR SEQ ID NO:3:	
87 88 89 90 91	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
93 94	(ii)	MOLECULE TYPE: DNA (genomic)	
95 96	(iii)	HYPOTHETICAL: NO	
97 98 99	(iv)	ANTI-SENSE: NO	

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100					
101					
102	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:				
103					
104	TGGATATTGC CATCAATGAC C	21			
105	(0) 7070000				
106	(2) INFORMATION FOR SEQ ID NO:4:				
107	(;) anathran arrangementanta				
108	(i) SEQUENCE CHARACTERISTICS:				
109	(A) LENGTH: 22 base pairs				
110	(B) TYPE: nucleic acid (C) STRANDEDNESS: double				
111 112	(-,				
112	(D) TOPOLOGY: linear				
113	(ii) MOLECULE TYPE: DNA (genomic)				
114	(II) MOLECOLE TIPE: DNA (Genomic)				
116	(iii) HYPOTHETICAL: NO				
117	(III) RIPOIREIICAL: NO				
118	(iv) ANTI-SENSE: NO				
119	(IV) ANII-SENSE: NO				
120					
121					
122					
123	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:				
124	(XI) DECORNCE DESCRIPTION. DEQ ID NO.1.				
125	GATGGCATGG ACTGTGGTCA TG	22			
126					
127	(2) INFORMATION FOR SEQ ID NO:5:				
128					
129	(i) SEQUENCE CHARACTERISTICS:				
130	(A) LENGTH: 48 base pairs				
131	(B) TYPE: nucleic acid				
132	(C) STRANDEDNESS: double				
133	(D) TOPOLOGY: linear				
134					
135	(ii) MOLECULE TYPE: DNA (genomic)				
136					
137	(iii) HYPOTHETICAL: NO				
138					
139	(iv) ANTI-SENSE: NO				
140					
141					
142					
143					
144	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:				
145					
146	GGCTCATCCG GTCGACGAAT CAGACAAGTG AGTATGAAGG GTAGTAAG 48				
147	(2) INFORMATION FOR CEO ID NO C				
148	(2) INFORMATION FOR SEQ ID NO:6:				
149 150	(i) CEOUENCE CHADACTEDICTICS				
150	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 34 base pairs				
151	(B) TYPE: nucleic acid				
132	(D) TIPE. MUCICIC ACIA				

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		INTO I DELL. DEPOUNT
153	(C) STRANDEDNESS: double	
154	(D) TOPOLOGY: linear	
155		
156	(ii) MOLECULE TYPE: DNA (genomic)	
157		
158	(iii) HYPOTHETICAL: NO	
159		
160	(iv) ANTI-SENSE: NO	
161		
162		
163		
164		
165	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
166		
167	CTGCTGATAT CGCTGTCCCT CACAGGAGGG CGAG	34
168		

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